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ROBINS & PASTERNAK 1731 EMBARCADERO ROAD SUITE 230 PALO ALTO, CA 94303			WESSENDORF, TERESA D.	
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UNITED STATES PATENT AND TRADEMARK OFFICE

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BEFORE THE BOARD OF PATENT APPEALS  
AND INTERFERENCES

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*Ex parte* BRYAN S. WANG and CARL O. PABO

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Appeal 2010-008082  
Application 09/636,243  
Technology Center 1600

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Before ERIC GRIMES, DONALD E. ADAMS, and  
JEFFREY N. FREDMAN, *Administrative Patent Judges*.

ADAMS, *Administrative Patent Judge*.

DECISION ON APPEAL<sup>1</sup>

This appeal under 35 U.S.C. § 134 involves claims 5, 6, 20, and 21, the only claims pending in this application. We have jurisdiction under 35 U.S.C. § 6(b).

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<sup>1</sup> The two-month time period for filing an appeal or commencing a civil action, as recited in 37 C.F.R. § 1.304, or for filing a request for rehearing, as recited in 37 C.F.R. § 41.52, begins to run from the “MAIL DATE” (paper delivery mode) or the “NOTIFICATION DATE” (electronic delivery mode) shown on the PTOL-90A cover letter attached to this decision.

### STATEMENT OF THE CASE

The claims are directed to a zinc finger complex. Claim 5 is representative and is reproduced in the “Claims Appendix” of Appellants’ Brief (App. Br. 12).

Claims 5, 6, 20, and 21<sup>2</sup> stand rejected under 35 U.S.C § 103(a) as unpatentable over the combination of Pomerantz<sup>3</sup> and Krylov.<sup>4</sup>

We reverse.

### ISSUE

Does the preponderance of evidence support a conclusion that the combination of Pomerantz and Krylov suggests non-naturally occurring peptide linkers of 30 amino acids or less in length?

### FINDINGS OF FACT

FF 1. Claim 5 requires non-naturally occurring peptide linkers of 30 amino acids or less in length (Claim 5).

FF 2. The Examiner finds that “Pomerantz shows at the bottom panel [of Figure 1, page 968] that the dimerization domain is from 41 to 65 residues (i.e., 24 amino acid residues) in length” (Ans. 6).

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<sup>2</sup> In the Final Rejection the Examiner included claim 21 in this rejection (Fin. Rej. 2). Nevertheless, while the Examiner recognizes that claim 21 is on appeal (Ans. 2), the Examiner failed to include this claim in the statement of the rejection (Ans. 3). Appellants, however, identify claim 21 as part of the rejection of record (*see* App. Br. 3 and Reply Br. 2). Accordingly, we find the Examiner’s failure to include claim 21 in the statement of the rejection to be a typographical error and have included claim 21 in our deliberations on the rejection before us on Appeal.

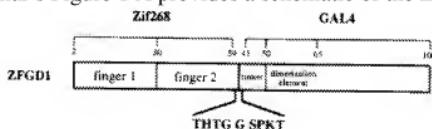
<sup>3</sup> Joel L. Pomerantz, et al., *Structure-Based Design of a Dimeric Zinc Finger Protein*, 37 BIOCHEMISTRY 965-970 (1998).

<sup>4</sup> Dmitry Krylov et al., *A thermodynamic scale for leucine zipper stability and dimerization specificity: e and g interhelical interactions*, 13 EMBO J. 2849-2861 (1994).

FF 3. Pomerantz constructed a fusion protein (ZFGD1) comprising zinc fingers 1 and 2 of Zif268 with a linker and a dimerization element consisting of residues 41-100 of GAL4 (Pomerantz 967: col. 1, ll. 38-39; *see also* Ans. 7).

FF 4. Pomerantz teaches that while “[s]tructural information is not available for residues 66-100 of GAL4 . . . these residues were included because they are known to form part of the GAL4 dimerization domain” (Pomerantz 967: col. 1, ll. 40-42).

FF 5. Pomerantz’s Figure 1 A provides a schematic of the ZFGD1 construct:



The foregoing schematic “indicat[es] the domain structure and linker region of ZFGD1” (Pomerantz 968: Figure 1).

FF 6. The Examiner finds that Krylov “teaches a [sic] coiled coil heptads, which is 24 amino acids long commencing from letter d (leucine) of the coiled-coil repeating heptad sequence (at most 29 of the coiled-coil interacting domain)” (Ans. 10).

FF 7. The Examiner finds that Krylov teaches:

(B) The amino acid sequence of the leucine zipper region of VBP is presented using the single-letter code. Below the VBP sequence is the nomenclature for the positions in a coiled coil. The sequence starts at the first ‘leucine’ position as defined previously (Vinson et al. 1989) and is grouped into heptads (g, a, b, [c], d, e, f).

(Ans. 10, quoting Krylov 2850: Fig 1. legend.)

FF 8. Krylov teaches that “[t]he protein sequence of the first four leucine zipper heptads of . . . bZIP protein VBP [the chicken version of the mammalian DBP] is presented in Figure 1B” reproduced below:

**B**

Heptad	1	2	3	4		
	g+t+e+	g+t+e+	g+t+e+	g+t+e+		
VBP	STI	RASPLER	MNTALERT	MVPAEAK	MVGRCOONI	
coiled coil	gabdef	gabdef	gabdef	gabdefg		
E-R	R	E	E	R	E	R
E-K <sub>4</sub>	R	E	B	R	E	R
E-R <sub>14</sub>	R	E	B	R	E	K
E-K <sub>1234</sub>	Z	S	E	K	R	K
Q-E <sub>1234</sub>	E	Q	Q	R	Q	R

“The amino acid sequence of the leucine zipper region of VBP . . . is presented using the single-letter code. Below the VBP sequence is the nomenclature for the positions in a coiled coil” (Krylov 2850: Fig. 1, legend).

## ANALYSIS

Claim 5 requires non-naturally occurring peptide linkers of 30 amino acids or less in length (FF 1).

Contrary to the Examiner’s assertion (FF 2) we agree with Appellants’ contention that “[t]he GAL4 dimerization domain used in Pomerantz is fully 50 amino acids in length . . . [and] this does not include a 9 amino acid peptide linker used to join the zinc fingers to the dimerization domain” (App. Br. 5; FF 3-5).

Contrary to the Examiner’s assertions (FF 6-7) we agree with Appellants’ contention that “Krylov’s dimerization domains are at least 3[3] amino acids in length (4 heptads and 3 N-terminus amino acids and 2 C-terminal amino acids)” (App. Br. 6; FF 8; *see also* Reply Br. 8). The Examiner asserts that Krylov’s leucine zipper dimerization domain begins with the leucine present in the first heptad of Krylov’s VBP protein (FF 6).

In support of this assertion the Examiner asserts that Krylov teaches that “[t]he sequence starts at the first ‘leucine’ position as defined previously (Vinson et al. 1989) and is grouped into heptads (g, a, b, [c], d, e, f)” (FF 7). The Examiner does not, however, establish that “the first ‘leucine’ position” defined by Vinson et al., is the leucine set forth in Krylov’s first heptad. In this regard, we note that Krylov states that “[t]he leucine positions are italicized” (Krylov 2850: Fig. 1, legend). We find that Appellants have the better argument, specifically that “the italicized [sic] ‘I’ residue of Figure 1B . . . acts as ‘leucine’ before the first heptad” (*see Reply Br.* 8).

The Examiner has provided no evidence or reasoning which suggests the use of peptide linkers of 30 amino acids or less in length in the zinc finger complex. Without such evidence or reasoning, we are constrained to reverse the rejection.

#### **CONCLUSION OF LAW**

The preponderance of evidence fails to support a conclusion that the combination of Pomerantz and Krylov suggests non-naturally occurring peptide linkers of 30 amino acids or less in length.

The rejection of claims 5, 6, 20, and 21 under 35 U.S.C § 103(a) as unpatentable over the combination of Pomerantz and Krylov is reversed.

**REVERSED**

cdc

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